

SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD

<120> An agent for prevention and/or treatment of asthma

<130> 11504W01

<140>

<141>

<150> JP 2002/241523

<151> 2002-08-22

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 1

tcgacaaata aagcaatagc atcacaaatt tcacaaataa agcatttttt tcaa 54

<210> 2

<211> 54

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

<400> 2

tgcatgaaa aaaatgcttt atttgtaaa ttgtgatgc tattgcttta ttg 54

<210> 3

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

<400> 3

tgcatctag ttgtggttg tccaaactcg agcccgggg 39

<210> 4

<211> 39

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

<400> 4

giacccccgg gctcgagttt ggacaaacca caactagaa 39

<210> 5

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

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tcgacggat cgattcgact gacgtcatac ttgacgtcac

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<210> 6

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

<400> 6

tcgagtgcg tcaagtatga cgtcagtcga atcgataccg

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<210> 7

<211> 29

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

<400> 7

gccccagaag cttaagtgcc caccatggg

29

<210> 8

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 8

gttcattgtg gcggccgcag catcttcagc tgc

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<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

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cggagactct agagggtata taatg

25

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

<400> 10

ctaatacgac tcactatagg g

21

<210> 11

<211> 362

<212> PRT

<213> Homo sapiens

<400> 11

Met Gly Asn His Thr Trp Glu Gly Cys His Val Asp Ser Arg Val Asp  
1 5 10 15

His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu  
20 25 30

Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln  
35 40 45

Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu  
50 55 60

Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His  
65 70 75 80

Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile  
85 90 95

Phe Tyr Thr Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser  
100 105 110

Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu  
115 120 125

Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr  
130 135 140

Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg  
145 150 155 160

Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly  
165 170 175

Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe  
180 185 190

Pro Trp Ala Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val  
195 200 205

Arg Gly Ser Val Ser Thr Glu Arg Gln Glu Lys Ala Lys Ile Lys Arg  
210 215 220

Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr  
225 230 235 240

His Val Leu Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp  
245 250 255

Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu  
260 265 270

Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu  
275 280 285

Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu  
290 295 300

Leu Arg Phe Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser  
305 310 315 320

Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys  
325 330 335

Ala Met Thr Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln  
340 345 350

Val Gln Leu Lys Met Leu Pro Pro Ala Gln  
355 360

<210> 12  
 <211> 2932  
 <212> DNA  
 <213> Homo sapiens

<400> 12

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agaccttact cactccttc ctgttctcta agactccttc ctgccgtcca cagaccgagc 180
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gtatttcttg tgtcttctag aacattcccc cgccattatt acttcaatat ggctacacat 420
acttctaat tgccctgcaa accatctct tctcaccatt gcccagcat gctttcgtct 480
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actgactcca tacataacct ccttgaaaaa cctctttatt aatctacca tcttcagac 600
ttccctctg tcataattcc atccctcttc caacttttcc ctctcaagct ctgcccttc 660
cagcccagcc cagcttacc aacctatct ctccctgtg gaccacatcc caccatgttc 720
ccctgagcct ccaaggaagg ggctcaggg gcccattggc ctcccgctcc ctgtggcccc 780
acagcccccg tgggccaggg gaagcgcccc agaagccgaa gtgcccacc atg ggc aac 838

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Met Gly Asn

1

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cac acg tgg gag ggc tgc cac gtg gac tgc cgc gtg gac cac etc ttt 886
His Thr Trp Glu Gly Cys His Val Asp Ser Arg Val Asp His Leu Phe
5 10 15

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ccg cca tcc etc tac atc ttt gtc atc ggc gtg ggg ctg ccc acc aac 934
Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu Pro Thr Asn
20 25 30 35

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tgc ctg gct ctg tgg gcg gcc tac cgc cag gtg caa cag cgc aac gag 982
Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln Arg Asn Glu
40 45 50

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ctg ggc gtc tac ctg atg aac ctc agc atc gcc gac ctg ctg tac atc 1030  
 Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu Leu Tyr Ile

55

60

65

tgc acg ctg ccg ctg tgg gtg gac tac ttc ctg cac cac gac aac tgg 1078  
 Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His Asp Asn Trp

70

75

80

atc cac ggc ccc ggg tcc tgc aag ctc ttt ggg ttc atc ttc tac acc 1126  
 Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile Phe Tyr Thr

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90

95

aat atc tac atc agc atc gcc ttc ctg tgc tgc atc tgc gtg gac cgc 1174  
 Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser Val Asp Arg

100

105

110

115

tac ctg gct gtg gcc cac cca ctc cgc ttc gcc cgc ctg cgc cgc gtc 1222  
 Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu Arg Arg Val

120

125

130

aag acc gcc gtg gcc gtg agc tcc gtg gtc tgg gcc acg gag ctg ggc 1270  
 Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr Glu Leu Gly

135

140

145

gcc aac tgc gcg ccc ctg ttc cat gac gag ctc ttc cga gac cgc tac 1318  
 Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg Asp Arg Tyr

150

155

160

aac cac acc ttc tgc ttt gag aag ttc ccc atg gaa ggc tgg gtg gcc 1366  
 Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly Trp Val Ala

165

170

175

tgg atg aac ctc tat cgg gtg ttc gtg gcc ttc ctc ttc ccg tgg gcg 1414  
 Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe Pro Trp Ala

180

185

190

195



ctc atg ctg ctg tgc tac cgg ggc atc ctg cgg gcc gtg cgg ggc agc 1462  
 Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val Arg Gly Ser  
                   200                                   205                                   210

gtg tcc acc gag cgc cag gag aag gcc aag atc aag cgg ctg gcc ctc 1510  
 Val Ser Thr Glu Arg Gln Glu Lys Ala Lys Ile Lys Arg Leu Ala Leu  
                   215                                   220                                   225

agc ctc atc gcc atc gtg ctg gtc tgc ttt gcg ccc tat cac gtg ctc 1558  
 Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr His Val Leu  
                   230                                   235                                   240

tig ctg tcc cgc agc gcc atc tac ctg ggc cgc ccc tgg gac tgc ggc 1606  
 Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp Asp Cys Gly  
                   245                                   250                                   255

ttc gag gag cgc gtc ttt tct gca tac cac agc tca ctg gct ttc acc 1654  
 Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu Ala Phe Thr  
                   260                                   265                                   270                                   275

agc ctc aac tgt gtg gcg gac ccc atc ctc tac tgc ctg gtc aac gag 1702  
 Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu Val Asn Glu  
                   280                                   285                                   290

ggc gcc cgc agc gat gtg gcc aag gcc ctg cac aac ctg ctc cgc ttt 1750  
 Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu Leu Arg Phe  
                   295                                   300                                   305

ctg gcc agc gac aag ccc cag gag atg gcc aat gcc tgc ctc acc ctg 1798  
 Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser Leu Thr Leu  
                   310                                   315                                   320

gag acc cca ctc acc tcc aag agg aac agc aca gcc aaa gcc atg act 1846  
 Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys Ala Met Thr  
                   325                                   330                                   335

ggc agc tgg gcg gcc act ccg ccc tcc cag ggg gac cag gtg cag ctg 1894  
 Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln Val Gln Leu  
 340 345 350 355

aag atg ctg ccg cca gca caa tga accccgagtg gcacagaatc cccagttttc 1948  
 Lys Met Leu Pro Pro Ala Gln  
 360

ccctctcatt ccacagtcct tctctctctg gctctgggtgta tgcaaattgt atggaaaaag 2008  
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 aaatatgtaa tgtttggaat tgct 2932

<210> 13

<211> 365

<212> PRT

<213> Mus musculus

<400> 13

Met Asp Asn Ser Thr Gly Thr Gly Glu Gly Cys His Val Asp Ser Arg

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Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val  
20 25 30

Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val  
35 40 45

Arg Gln His Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala  
50 55 60

Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu  
65 70 75 80

His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly  
85 90 95

Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys  
100 105 110

Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala  
115 120 125

Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp  
130 135 140

Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu  
145 150 155 160

Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met  
165 170 175

Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe  
180 185 190

Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg  
195 200 205

Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile  
210 215 220

Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala  
225 230 235 240

Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg  
245 250 255

Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser  
260 265 270

Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr  
275 280 285

Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His  
290 295 300

Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn  
305 310 315 320

Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr  
325 330 335

Gly Lys Ser Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly  
340 345 350

Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln  
355 360 365

<210> 14

<211> 1098

<212> DNA

<213> Mus musculus

<400> 14

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gtg gac cac ctc ttc cca cca tct ctc tac atc ttc gtc atc ggg gtg 96

Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val

20

25

30

ggg ctg ccc acc aac tgc ctg gcc ctg tgg gca gcc tac cgg cag gtg 144

Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val

35

40

45

cgc caa cac aat gag ctg ggc gtc tac ctg atg aac ttg agc att gca 192

Arg Gln His Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala

50

55

60

gac ctg ctg tac atc tgc act ttg ccg ctg tgg gtc gac tac ttc ctc 240

Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu

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70

75

80

cac cat gac aac tgg atc cac ggc cct ggc tcc tgc aag ctc ttt ggc 288

His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly

85

90

95

ttc atc ttc tac agc aac atc tat atc agc atc gcc ttc ctg tgc tgc 336

Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys

100

105

110

atc tcc gtg gac cgc tac ctg gct gtg gct cat cct ctg cgc ttt gca 384

Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala

115

120

125

cgc ctg cgc cgg gtc aag aca gca gtg gct gtg agc tct gtg gtc tgg 432

Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp

130

135

140

gcc acg gag ctg ggc gcc aat tca gca ccg ctc ttc cat gat gag ctg 480  
 Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu

145

150

155

160

ttt cgt gat cgc tac aac cac acc ttc tgc ttt gag aag ttc ccc atg 528  
 Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met

165

170

175

gag cgt tgg gtg gcc tgg atg aat ctg tac cgc gtc ttt gtg ggc ttc 576  
 Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe

180

185

190

ctc ttc ccc tgg gca ctc atg ttg ctg tgc tac cgt ggc atc ctg agg 624  
 Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg

195

200

205

gca gtg cag agc agt gtg tcc acc gag cgc cag gag aaa gtc aag atc 672  
 Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile

210

215

220

aaa cgt ctg gcc ctg agc ctc atc gcc att gtg ctg gtg tgc ttt gcg 720  
 Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala

225

230

235

240

cct tac cat gct ctc ctg ctg tct cgc agc gcc gtc tac ctg ggc cgg 768  
 Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg

245

250

255

ccc tgg gac tgt ggc ttc gag gag cga gtc ttt tct gcc tac cac agc 816  
 Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser

260

265

270

tcc ctg gcc ttc acc agc ctc aat tgt gtg gct gac ccc atc ctc tac 864  
 Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr

275

280

285

tgc ctg gtc aac gag ggt gcc cgc agt gat gtg gcc aag gcc ctg cac 912  
 Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His  
 290 295 300

aac ctc ctc cgc ttc ctg gcc agc aac aag ccc cag gag atg gcc aat 960  
 Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn  
 305 310 315 320

gct tcc ctc acc ctg gag aca ccc ttg acc tcc aag agg agc acc acc 1008  
 Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr  
 325 330 335

ggc aag tgc tcc ggg gct gtc tgg gca gtg cct ccg act gcc cag ggg 1056  
 Gly Lys Ser Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly  
 340 345 350

gac cag gtg cca ctg aag gtg ctg ctg ccc ccg gca cag tga 1098  
 Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln  
 355 360 365

&lt;210&gt; 15

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: synthetic DNA

&lt;400&gt; 15

ataagcttgccaccatggacaacagcacgggcac

36

&lt;210&gt; 16

&lt;211&gt; 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 16

tagcgccgctcactgtgccgggggcagcag

33

<210> 17

<211> 365

<212> PRT

<213> Rattus norvegicus

<400> 17

Met Asp Asn Ser Thr Gly Thr Trp Glu Gly Cys His Val Asp Ser Arg  
1 5 10 15

Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val  
20 25 30

Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val  
35 40 45

Arg Gln Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala  
50 55 60

Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu  
65 70 75 80

His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly  
85 90 95

Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys  
100 105 110



Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala  
115 120 125

Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp  
130 135 140

Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu  
145 150 155 160

Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met  
165 170 175

Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe  
180 185 190

Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg  
195 200 205

Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile  
210 215 220

Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala  
225 230 235 240

Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg  
245 250 255

Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser  
260 265 270

Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr  
275 280 285

Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His  
290 295 300

Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn  
 305 310 315 320

Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr  
 325 330 335

Gly Lys Thr Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly  
 340 345 350

Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln  
 355 360 365

<210> 18

<211> 1098

<212> DNA

<213> Rattus norvegicus

<400> 18

atg gac aac agc acg ggc acg tgg gag ggc tgc cat gtg gac tct cga 48  
 Met Asp Asn Ser Thr Gly Thr Trp Glu Gly Cys His Val Asp Ser Arg  
 1 5 10 15

gtg gac cac ctc ttc cca cca tcc ctc tac atc ttc gtc atc ggg gtg 96  
 Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val  
 20 25 30

ggg ctg ccc acc aac tgc ctg gcc ctg tgg gca gcc tac cgc cag gtg 144  
 Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val  
 35 40 45

cgc cag cgc aat gag ctg ggc gtc tac ctg atg aac ttg agc atc gca 192  
 Arg Gln Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala  
 50 55 60

gac ctg ctg tac atc tgt acg ctg ccg ctg tgg gtc gac tac ttc ctc 240



Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile	
210 215 220	
aaa cgc ctg gcc ctg agc ctc atc gcc atc gtg ctg gtg tgc ttt gca	720
Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala	
225 230 235 240	
ccc tac cat gct ctc ttg ctg tct cgc agc gct gtc tat ctg ggc cgg	768
Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg	
245 250 255	
ccc tgg gac tgt ggc ttc gag gag cga gtc ttc tct gcc tac cac agc	816
Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser	
260 265 270	
tcc cta gcc ttc acc agc ctc aat tgc gtg gct gac ccc atc ctc tac	864
Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr	
275 280 285	
tgc ctg gtc aac gag ggt gcc cgt agt gac gtg gcc aaa gcc ctg cac	912
Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His	
290 295 300	
aac ctc ctc cgc ttc ctg gcc agc aac aag ccc cag gag atg gcc aat	960
Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn	
305 310 315 320	
gct tcc ctc acc ctg gag aca cca ttg acc tcc aag agg agc acc acc	1008
Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr	
325 330 335	
ggc aaa acg tct ggg gct gtc tgg gca gtg cct ccc act gcc cag ggg	1056
Gly Lys Thr Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly	
340 345 350	
gac cag gtg cca ctg aag gig ctg ctg ccc ccg gca cag tga	1098

Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln  
355 360 365